

SEQUENCE LISTING

(110) Lorenz, M., et al.

(120) A NOVEL P-SELECTIN GLYCOPROTEIN LIGAND (PSGL-1)
BINDING PROTEIN AND USES THEREFOR

(130) GFN-5380

(140)

(141)

(150) 60/192,104

(161) 2000-03-24

(160) 4

(170) PatentIn Ver. 2.0

(210) 1

(211) 951

(212) DNA

(213) Homo sapiens

(220)

(221) CDS

(222) (1)..(948)

(400) 1

atg gca agt cca gag cac cct ggg agc cct ggc tgc atg gga ccc ata	48
Met Ala Ser Pro Glu His Pro Gly Ser Pro Gly Cys Met Gly Pro Ile	
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acc cag tgc acg gca agg acc cag cag gaa gca cca gcc act ggc ccc	96
Thr Gln Cys Thr Ala Arg Thr Gln Gln Glu Ala Pro Ala Thr Gly Pro	
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gac ctg ccg cac cca gga cct gac ggg cac tta gac aca cac agt ggc	144
Asp Leu Pro His Pro Gly Pro Asp Gly His Leu Asp Thr His Ser Gly	
35 40 45	

ctg agc tcc aac tcc agc atg acc acg cgg gag ctt cag cag tac tgg	192
Leu Ser Ser Asn Ser Ser Met Thr Thr Arg Glu Leu Gln Gln Tyr Trp	
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cag aac cag aaa tgc cgc tgg aag cac gtc aaa ctg ctg ttt gag atc	240
Gln Asn Gln Lys Cys Arg Trp Lys His Val Lys Leu Leu Phe Glu Ile	
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gct tca gct cgc atc gag gag aga aaa gtc tct aag ttt gtg gtg tac	288
Ala Ser Ala Arg Ile Glu Glu Arg Lys Val Ser Lys Phe Val Val Tyr	
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caa atc atc gtc atc cag act ggg agc ttt gac aac aac aag gcc gtc	336
Gln Ile Ile Val Ile Gln Thr Gly Ser Phe Asp Asn Asn Lys Ala Val	
100 105 110	

ctg gaa cgg cgc tat tcc gac ttc ggc aag ctg cag aaa gcc ctg ctg	384
Leu Glu Arg Arg Tyr Ser Asp Phe Ala Lys Leu Gln Lys Ala Leu Leu	
115 120 125	

aag acg ttc agg gag gag atc gaa gac gtg gag ttt ccc agg aag cac 432
Lys Thr Phe Arg Glu Glu Ile Glu Asp Val Glu Phe Pro Arg Lys His
130 135 140

ctg act ggg aac ttc gct gag gag atg atc tgt gag cgt cgg cgc gcc 440
Leu Thr Gly Asn Phe Ala Glu Glu Met Ile Cys Glu Arg Arg Arg Ala
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Leu Gln Glu Tyr Leu Gly Leu Leu Tyr Ala Ile Arg Cys Val Arg Arg
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tcc cgg gag ttc ctg gac ttc ctc acg cgg ccg gag ctg cgc gag gct 516
Ser Arg Glu Phe Leu Asp Phe Leu Thr Arg Pro Glu Leu Arg Glu Ala
180 185 190

ttc ggc tgc ctg cgg gcc ggc cag tac ccg cgc gcc ctg gag ctg ctg 624
Phe Gly Cys Leu Arg Ala Gly Gln Tyr Pro Arg Ala Leu Glu Leu Leu
195 200 205

ctg cgc gtg ctg ccg ctg cag gag aag ctc acc gcc cac tgc cct gcg 672
Leu Arg Val Leu Pro Leu Gln Glu Lys Leu Thr Ala His Cys Pro Ala
210 215 220

gcc gcc gtc ccg gcc ctg tgc gcc gtg ctg ctg tgc cac cgc gac ctc 720
Ala Ala Val Pro Ala Leu Cys Ala Val Leu Leu Cys His Arg Asp Leu
225 230 235 240

gac cgc ccc gcc gag gcc ttc gcg gcc gga gag agg gcc ctg cag cgc 768
Asp Arg Pro Ala Glu Ala Phe Ala Ala Gly Glu Arg Ala Leu Gln Arg
245 250 255

ctg cag gcc cgg gag ggc cat cgc tac tat gcg cct ctg ctg gac gcc 816
Leu Gln Ala Arg Glu Gly His Arg Tyr Tyr Ala Pro Leu Leu Asp Ala
260 265 270

atg gtc cgc ctg gcc tac gcg ctg ggc aag gac ttc gtg act ctg cag 864
Met Val Arg Leu Ala Tyr Ala Leu Gly Lys Asp Phe Val Thr Leu Gln
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gag agg ctg gag gag agc cag ctc cgg agg ccc acg ccc cga gcc atc 912
Glu Arg Leu Glu Glu Ser Gln Leu Arg Arg Pro Thr Pro Arg Gly Ile
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<113> Homo sapiens

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 Leu Ser Ser Asn Ser Ser Met Thr Thr Arg Glu Leu Gln Gln Tyr Trp
 50 55 60
 Gln Asn Gln Lys Cys Arg Trp Lys His Val Lys Leu Leu Phe Glu Ile
 65 70 75 80
 Ala Ser Ala Arg Ile Glu Glu Arg Lys Val Ser Lys Phe Val Val Tyr
 85 90 95
 Gln Ile Ile Val Ile Gln Thr Gly Ser Phe Asp Asn Asn Lys Ala Val
 100 105 110
 Leu Glu Arg Arg Tyr Ser Asp Phe Ala Lys Leu Gln Lys Ala Leu Leu
 115 120 125
 Lys Thr Phe Arg Glu Glu Ile Glu Asp Val Glu Phe Pro Arg Lys His
 130 135 140
 Leu Thr Gly Asn Phe Ala Glu Glu Met Ile Cys Glu Arg Arg Arg Ala
 145 150 155 160
 Leu Gln Glu Tyr Leu Gly Leu Leu Tyr Ala Ile Arg Cys Val Arg Arg
 165 170 175
 Ser Arg Glu Phe Leu Asp Phe Leu Thr Arg Pro Glu Leu Arg Glu Ala
 180 185 190
 Phe Gly Cys Leu Arg Ala Gly Gln Tyr Pro Arg Ala Leu Glu Leu Leu
 195 200 205
 Leu Arg Val Leu Pro Leu Gln Glu Lys Leu Thr Ala His Cys Pro Ala
 210 215 220
 Ala Ala Val Pro Ala Leu Cys Ala Val Leu Leu Cys His Arg Asp Leu
 225 230 235 240
 Asp Arg Pro Ala Glu Ala Phe Ala Ala Gly Glu Arg Ala Leu Gln Arg
 245 250 255
 Leu Gln Ala Arg Glu Gly His Arg Tyr Tyr Ala Pro Leu Leu Asp Ala
 260 265 270
 Met Val Arg Leu Ala Tyr Ala Leu Gly Lys Asp Phe Val Thr Leu Gln
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<213> Artificial Sequence

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(223) Description of Artificial Sequence: primer

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(210) 4

(211) 33

(212) INA

(213) Artificial Sequence

(220)

(223) Description of Artificial Sequence: primer

(400) 4

atacaggatc cagagtgagc taagggagga aag

33

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